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OM protein - protein search, using sw model

Run on: June 9, 2003, 07:07:25 ; Search time 19 Seconds
(without alignments)
583.813 Million cell updates/sec

Title: US-10-091-628-2
Perfect score: 1979
Sequence: 1 MRANSSSSACAPANSSEBEL.....PGPMCHRALPVGHTSC 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
ched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	884	44.7	348	1	US-08-176-126B-2
2	884	44.7	348	2	US-08-669-435-2
3	884	44.7	348	5	PCT-US94-14431A-2
4	860.5	43.5	348	1	US-08-176-126B-4
5	860.5	43.5	348	2	US-08-669-435-4
6	860.5	43.5	348	5	PCT-US94-14431A-4
7	101	5.1	370	4	US-08-405-271A-21
8	100.5	5.1	424	4	US-09-134-001C-5009
9	99.5	5.0	387	4	US-08-993-088A-7
10	99.5	5.0	387	4	US-08-993-424B-7
11	98.5	5.0	344	3	US-09-110-116-4
12	98	5.0	835	4	US-09-284-819-6
13	96.5	4.9	3177	2	US-08-477-451-4
14	96	4.9	521	4	US-08-956-322-4
15	96	4.9	572	4	US-08-937-067-13
16	96	4.9	652	4	US-09-110-116-1
17	96	4.9	652	4	US-08-956-322-2
18	93	4.7	372	2	US-08-514-451A-9
19	93	4.7	372	4	US-09-048-916B-8
20	93	4.7	487	1	US-08-444-734A-2
21	93	4.7	532	1	US-08-140-729A-3
22	93	4.7	532	1	US-08-546-666-3
23	93	4.7	532	2	US-08-916-745-3
24	93	4.7	532	2	US-09-042-929-3
25	93	4.7	532	2	US-08-546-661-3
26	93	4.7	532	2	US-09-042-960-3
27	93	4.7	532	3	US-09-198-650-3

28	93	4.7	532	3	US-09-042-913-3	Sequence 3, Appli
29	93	4.7	532	3	US-09-042-937-3	Sequence 3, Appli
30	93	4.7	532	4	US-09-042-709A-3	Sequence 3, Appli
31	92.5	4.7	554	4	US-09-134-001C-5109	Sequence 3, Appli
32	92	4.6	683	4	US-09-134-001C-5576	Sequence 5576, Ap
33	91.5	4.6	367	2	US-08-454-552-4	Sequence 4, Appli
34	91.5	4.6	367	3	US-08-454-552-4	Sequence 4, Appli
35	91.5	4.6	367	3	US-08-676-351-3	Sequence 3, Appli
36	91.5	4.6	372	4	US-08-188-275A-4	Sequence 4, Appli
37	91.5	4.6	372	4	US-09-351-198-4	Sequence 4, Appli
38	91.5	4.6	372	4	US-09-113-426-4	Sequence 4, Appli
39	91.5	4.6	485	1	US-08-453-956-15	Sequence 15, Appli
40	91.5	4.6	485	1	US-08-086-631-15	Sequence 15, Appli
41	91.5	4.6	485	2	US-08-452-930-15	Sequence 15, Appli
42	91.5	4.6	485	5	PCT-US93-08174-15	Sequence 15, Appli
43	91	4.6	843	4	US-09-361-631-1	Sequence 1, Appli
44	90.5	4.6	405	4	US-09-134-001C-4999	Sequence 4999, Ap
45	90	4.5	372	3	US-09-170-331-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-176-126B-2
Sequence-2: Application: US/08176126B
Patent No. 5589358

GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,126B

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE:002/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-176-126B-2

Query Match 44.7% Score 884; DB 1; Length 348;

Best Local Similarity 46.9% Pred. No. 2.4e-82;

Matches: 164; Conservative: 74; Mismatches: 102; Indels: 10; Gaps: 4;

QY 7 SSSACAPANS--EEELPVGLEVHGN--LELVFTVSTVMGLMPSGCCSVEIRKMSHI 62
DB 3 NSSICNPATICEBDSICAPESNPAISVMSYTVLITLAVFMSMOCNVEHLKFLQHT 62
QY 63 RRPQIAVGLICQGLMFTAYLLAISFLKPVQIAVAVLINGCCPGGITSNIFFWVDGD 122

Db 63 RRPWGIIVGFLCOFGIMPLTGFVLSVAFGILPVOAVVLLIOGCCPGGTAISNLLAWVDGD 122
Qy 123 MDLSIMTCTSTVALAGMPLCIYLYTWSMSLQONLTIPYONIGITVCLTTPVAFGVV 182
Db 123 MDLSVMTCTSTLALAGMPLCLFYTKMWDGSIIVIPYDSIGSLVALVIPSIGMY 182
Qy 183 NYRWPQKSIILKIGAVGVLLVAVAGVVLAKGSNSDITLLTISFIPPLIGHVTGF 242
Db 183 NHKWPQKSIILKIGSIAGAILIYVAVGILVQSAMTIEPKLMIIGTIVPIAGYGLGF 242
Qy 243 LLALFTHSNORCRITSLFTGAONITMLOSTFAHLVOMLSFPLAGLPOLDIF 302
Db 243 FLARIAGQPMYRCRVALLETGLONTQLCSTIVQLSFSPEDLNVLVFTFPLIYSIFOLAFPA 302
Qy 303 LIVAAYQTYKRLKNHKGKNSGCTEVCHTRKS--TSRETNALFEVNEE 350
Db 303 ILGAVVAYKK-----CHGKNNTLEOKETDNEMEPRSSFOETNKGQPDKE 348

ULT 2

8-669-435-2 Application US/08669435
Sequence 2, Patent No. 5869265

GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,435

FILING DATE: 26-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE:002/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: na

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-669-435-2

Query Match 44.7%; Score 884; DB 2; Length 348;
Best Local Similarity 46.9%; Pred. NO. 2.4e-82;
Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy 63 RRPWGIIVGFLCOFGIMPLTGFVLSVAFGILPVOAVVLLIOGCCPGGTAISNLLAWVDGD 122
Db 63 RRPWGIIVGFLCOFGIMPLTGFVLSVAFGILPVOAVVLLIOGCCPGGTAISNLLAWVDGD 122
Qy 123 MDLSIMTCTSTVALAGMPLCIYLYTWSMSLQONLTIPYONIGITVCLTTPVAFGVV 182
Db 123 MDLSVMTCTSTLALAGMPLCLFYTKMWDGSIIVIPYDSIGSLVALVIPSIGMY 182
Qy 183 NYRWPQKSIILKIGAVGVLLVAVAGVVLAKGSNSDITLLTISFIPPLIGHVTGF 242
Db 183 NHKWPQKSIILKIGSIAGAILIYVAVGILVQSAMTIEPKLMIIGTIVPIAGYGLGF 242
Qy 243 LLALFTHSNORCRITSLFTGAONITMLOSTFAHLVOMLSFPLAGLPOLDIF 302
Db 243 FLARIAGQPMYRCRVALLETGLONTQLCSTIVQLSFSPEDLNVLVFTFPLIYSIFOLAFPA 302
Qy 303 LIVAAYQTYKRLKNHKGKNSGCTEVCHTRKS--TSRETNALFEVNEE 350
Db 303 ILGAVVAYKK-----CHGKNNTLEOKETDNEMEPRSSFOETNKGQPDKE 348

RESULT 3

PCT-US94-14431A-2
Sequence 2, Application PC/TUS9414431A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14431A

FILING DATE: 29-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE005P--

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924(1) GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-14431A-2

Query Match 44.7%; Score 884; DB 5; Length 348;
Best Local Similarity 46.9%; Pred. NO. 2.4e-82;
Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

QY 63 RRPWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 122
DB 63 RRPWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 122
QY 123 MDLSMTTCSITVAALGMPPLCIYLTWMSLQONITIPYONIGITVLCITPVAFGVYV 182
DB 123 MDLSMTTCSITVAALGMPPLCIYLTWMSLQONITIPYONIGITVLCITPVAFGVYV 182
QY 183 NVRWPKOSKIILKIGAVGVLLVAVAGVVLAKGSMSNDITLITISFIPPLIGHVTF 242
DB 183 NVRWPKOSKIILKIGAVGVLLVAVAGVVLAKGSMSNDITLITISFIPPLIGHVTF 242
QY 243 LALTFHOSQRCRTISLETGAONIQMCTMLQSLFPAHLVOMLSFPLAYGLFOLIDGF 302
DB 243 LALTFHOSQRCRTISLETGAONIQMCTMLQSLFPAHLVOMLSFPLAYGLFOLIDGF 302
QY 303 LIAVAVQYKRLKNGKNGSGCTEVCCHTKRS--TSSEETAFLAEVNEE 350
DB 303 LIAVAVQYKRLKNGKNGSGCTEVCCHTKRS--TSSEETAFLAEVNEE 350
QY 303 ILGAVVAYK---CHGNKNTLEQKTDNEMEPRESSFQETWKGFPQDEK 348
DB 303 ILGAVVAYK---CHGNKNTLEQKTDNEMEPRESSFQETWKGFPQDEK 348

RESULT 4

US-08-176-126B-4
Sequence: Application US/08176126B
Patent No. 5589358
GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.
TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,126B

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: MAKE:002/PAR

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: na

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-176-126B-4

Query Match 43.5% Score 860.5; DB 1; Length 348;
Best Local Similarity 45.6%; Pred. No. 6.2e-80;
Matches 160; Conservative 68; Mismatches 104; Indels 19; Gaps 4;

QY 5 CSSSACAPANSSEELPVGLVHGNLELFTVSTVMGLMFSIGCSVEIRKLSHRR 64
DB 14 CSGASCVPESNFNNI-----LSVLSVLTITLALVMSGCNVEIKKFLGHTR 64
QY 65 PWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 124
DB 65 PWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 124

QY 125 LLSMTTCSITVAALGMPPLCIYLTWMSLQONITIPYONIGITVLCITPVAFGVYV 184
DB 125 LLSMTTCSITVAALGMPPLCIYLTWMSLQONITIPYONIGITVLCITPVAFGVYV 184
QY 185 RWPKOSKIILKIGAVGVLLVAVAGVVLAKGSMSNDITLITISFIPPLIGHVTF 244
DB 185 RWPKOSKIILKIGAVGVLLVAVAGVVLAKGSMSNDITLITISFIPPLIGHVTF 244
QY 245 ALTFHOSQRCRTISLETGAONIQMCTMLQSLFPAHLVOMLSFPLAYGLFOLIDGF 304
DB 245 ALTFHOSQRCRTISLETGAONIQMCTMLQSLFPAHLVOMLSFPLAYGLFOLIDGF 304
QY 305 VAAVQYKRLKNGKNGSGCTEVCCHTKRS--TSSEETAFLAEVNEE 355
DB 305 VAAVQYKRLKNGKNGSGCTEVCCHTKRS--TSSEETAFLAEVNEE 355
QY 305 LGFVAVYK---CHGNKNTLEQKTDNEMEPRESSFQETWKGFPQDEK 345
DB 305 LGFVAVYK---CHGNKNTLEQKTDNEMEPRESSFQETWKGFPQDEK 345

RESULT 5

US-08-669-435-4
Sequence: Application US/08669435
Patent No. 5589358
GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.
TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,435

FILING DATE: 26-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: MAKE:002/PAR

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: na

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-669-435-4

Query Match 43.5% Score 860.5; DB 2; Length 348;
Best Local Similarity 45.6%; Pred. No. 6.2e-80;
Matches 160; Conservative 68; Mismatches 104; Indels 19; Gaps 4;

QY 5 CSSSACAPANSSEELPVGLVHGNLELFTVSTVMGLMFSIGCSVEIRKLSHRR 64
DB 14 CSGASCVPESNFNNI-----LSVLSVLTITLALVMSGCNVEIKKFLGHTR 64
QY 65 PWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 124
DB 65 PWGIAVGLLCQFGIMPTAVLLAIFSLKPVQALAVLIMGCCPGGTISNIFTFWVDGD 124

DB 65 PWGICVGLCGFIMPGLFPLISVAFDILPLQAVVLLIIGCCPGTASNLIAWVDGMD 124

QY 125 LSIAMTTCSTVAALGMPPLCIYLYTWSWLSQONLTIPIYONIGITLVCLTIPIVAFGVVNY 184

DB 125 LSVSMTTCSTLLALGMPPLCLLIYTKMWVDSGSIVIPYDNIGTSLVALVVPVSIQMPVNH 184

QY 185 RWPKOSKIIILKIGAVGVLLVAVAGVVLAKGSMNSDITLITSFIPPLIGHVTGFL 244

DB 185 RWPKOSKIIILKIGSISAGAILVILAVVGLIYQSMIAPKLMITGITFPVAGSLGFL 244

QY 245 ALFTHOSMORCFTISLETGAONIMQCTIMLQSFPAEHLVQMLSPFLAYGLFOLIDGFLI 304

DB 245 ARIAGLPWIRCKRVAFTGMQNTOLCSTIVQLSFTPELNVVTFPLIYSIFQLAPALF 304

QY 305 VAAVOTYKRLKXKXKXSGCTEVCHTRKSTSSRETNAFLVNEGAITP 355

DB 305 LGFYVAAYKK----CHGKXKAETPE----SKENGTEPSSFYKAN--GGFOP 345

RESULT 6

-US94-14431A-4

Sequence 4, Application PC/US9414431A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14431A

FILING DATE: 29-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE005P--

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924(1) GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-14431A-4

Query Match

Best Local Similarity 43.5%; Score 860.5; DB 5; Length 348;

Matches 160; Conservative 69; Mismatches 104; Indels 19; Gaps 4;

DB 14 CSASACVPEPNSNNI-----LSVLSITVLITLILALWMSGCNNEIKKFLSHIRK 64

QY 5 CSSSSACPNASSEELPVGLVHGNLELVFTVSTVMGMLMSLGCSEVIRKLSHIRK 64

DB 65 PMGIAVGLLCOFLMPFTAVLLAISPLKPVQAVLAVLIMCCPGGTISNFTFWVDGMD 124

DB 65 PWGICVGLCGFIMPGLFPLISVAFDILPLQAVVLLIIGCCPGTASNLIAWVDGMD 124

QY 125 LSIAMTTCSTVAALGMPPLCIYLYTWSWLSQONLTIPIYONIGITLVCLTIPIVAFGVVNY 184

DB 125 LSVSMTTCSTLLALGMPPLCLLIYTKMWVDSGSIVIPYDNIGTSLVALVVPVSIQMPVNH 184

QY 185 RWPKOSKIIILKIGAVGVLLVAVAGVVLAKGSMNSDITLITSFIPPLIGHVTGFL 244

DB 185 RWPKOSKIIILKIGSISAGAILVILAVVGLIYQSMIAPKLMITGITFPVAGSLGFL 244

QY 245 ALFTHOSMORCFTISLETGAONIMQCTIMLQSFPAEHLVQMLSPFLAYGLFOLIDGFLI 304

DB 245 ARIAGLPWIRCKRVAFTGMQNTOLCSTIVQLSFTPELNVVTFPLIYSIFQLAPALF 304

QY 305 VAAVOTYKRLKXKXKXSGCTEVCHTRKSTSSRETNAFLVNEGAITP 355

DB 305 LGFYVAAYKK----CHGKXKAETPE----SKENGTEPSSFYKAN--GGFOP 345

RESULT 7

US-08-405-271A-21

Sequence 21, Application US/08405271A

Patent No. 6432652

GENERAL INFORMATION:

APPLICANT: EVANS, CHRISTOPHER J.

APPLICANT: KEITH, DUANE E.

TITLE OF INVENTION: OPTOID RECEPTOR GENES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/405,271A

FILING DATE: 14-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20526.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030 MRSNFOERSWSH

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 370 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURES:

NAME/KEY: Modified-site

LOCATION: group(18, 33)

OTHER INFORMATION: /note="extracellular Asn residues

OTHER INFORMATION: that are consensus sites for N-linked glycosylation"

US-08-405-271A-21

Query Match

Best Local Similarity 5.1%; Score 101; DB 4; Length 370;

Matches 91; Conservative 58; Mismatches 147; Indels 124; Gaps 22;

DB 17 ANASDAVYSACPSAGANNS-----GPARASASIALAIATTA-----LTSVAVCAV----- 61

QY 3 ANCSSS--SACP--ANSSEELPVGLVHGNLELVFTVSTVMGMLMSLGCSEVIRK 57

QY 58 LMSHRRPWGIAVGLLQFGLMPFTAYLIAIS---FSIKPVOAIAVLIMGCCPGTISNI 114
DB 62 -----GLIGNVLVWGVIVRYTKMKATNIYIFNLALADALNSTL---PFSAKTL 109
QY 115 FTFWGDMDLSISMTTSTVALGMPCLITYTWSLSQONLTIPYONIGITLVCLT- 173
DB 110 METWPFGEI-----LCKAV-----LSIDVYMFSTISFTILM 140
QY 174 -----IVARGV-VYVYRWPQSKII---LKIGAVGVLVAVVA---GVLA--- 216
DB 141 MSVDRIYAVCHPVDKALDFETPAKALINICIVWLASGVGVPMWAVTRPRDGAVVCMLQ 200
QY 217 --KGSWNSD---ITLITISFIFPLIGHVTFLLAFTQSWQCRKISLETGAONIMC 270
DB 201 FSPSWMDVTVKICVPLFAFVPLIITVCGLML-----RARSVLSSGSKEXORS 254
QY 271 ---ITMLOLSTAEHLV---OMLSFPLAVGLFOLIDFLIYAAYOTYKRLKNKKGKONS 324
DB 255 LRRITRMVLVVGAFVVCAPPIHIVITVTLDIRDPLVVAAL-----HLCIALGVANS 309
QY 325 GCTEVCHTRKSTSSRETNAFLEVNREGAITP-----GPPGMDCHRALEPVG--HITSC 376
DB 310 SLNPLY-----AFIDENFKRCFRQLCRKPCGPPDSSFSRAEATARERVTAC 358

RESULT 8

US-09-134-001C-5009

Sequence 5009, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5009

LENGTH: 424

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5009

Query Match 5.1%; Score 100.5; DB 4; Length 424;

Best Local Similarity 28.4%; Pred. No. 0.05;

Matches 55; Conservative 30; Mismatches 74; Indels 35; Gaps 11;

QY 32 LVFTVSTVVMGMLNFSIG---CSVEIRKL-WSHIRPW---GIAVGLLQFGLMPFT 82
DB 228 LVFFIVAVVS---LLESTGVYHALSEITGRKLERKDFRGKYAEGLAIIIGSIFNAFPYT 284
QY 83 AY-----LLAISFSFKP---VQATAVILMGCCPG-GTISNFTFWV-DGMDLSISMTT 131
DB 285 AYSQNVGLVUSGAKKNVITYGMVILLICGICPKLAGALANIIPLPVGGAIAMFGWMM 344
QY 132 CSTVALGMPCLITYTWSLSQONLTIPYONIGITLVCLTIPYAF-GVYVYVYRWPQKS 190
DB 345 AYGVGIIILNI-----NFGONNLLIATISVGLAGISAVPAQFGLSGQFAMLQN 395
QY 191 KIILKIGAVGVVL 204
DB 386 GIVL--GAISATIL 407

RESULT 9

US-08-993-088A-7

Sequence 7, Application US/08993088A

Patent No. 6287855

GENERAL INFORMATION:

APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,088A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 19846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1958
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-088A-7

Query Match 5.0%; Score 99.5; DB 4; Length 387;

Best Local Similarity 20.8%; Pred. No. 0.056;

Matches 73; Conservative 47; Mismatches 118; Indels 113; Gaps 18;

QY 109 GTISN-IFTFWVDGMDLSISMTTCTSTVALGMPCLITYTWSLSQONLTIPYONIG 166
DB 39 GTVGNTVLAVILRGQAVS---TTNLFILMIGVADLCFIL-----CVVFPQATI 85
QY 167 IT-----LVCLTI-----PVAFGVYVYRWPQKSK-----ITLK 195
DB 86 YLLDGVWVSGLLCKAVHFLIFLWMASSFTLAASLDRIYLRPLHSREIRTPRNALAA 145
QY 196 IGAVVGVLIL- -VVAAGVVLAKGSWNS-----DTLITISFIFPLIGHT 240
DB 146 IGLWGLSLLSGPRYLSYRQSLANLTVCHPANSAPRRAMDICTFVFSVLEPLV--VL 203
QY 241 GFLALFTQSWQCRKISLETGAONIMCITMLOLSTFA-----EHLVQML-----S 288
DB 204 GLTYAKRLRYLRAVDPAAGSAGARRAKYTRMILIVAAFLCWMPHHALILCVMPGQ 263
QY 289 FPLAVGLFQLIDGLFLIYAAYOTYK-----RLKNKKGKN-----S 324
DB 264 FPLTRATYAL--RILSHLVSVANSVNPVYVALVSHFRKGFERTTACGLGRAPGRAS 319
QY 325 GCTEVCHTRKSTSS---RETNAFLEVNE-EGAITPQPPGMDCHRALEP 369
DB 320 G--RVCAARGTGSGSVLERESSDLNHSALGALRPGASQPC--ILPP 366

RESULT 10

US-08-993-424B-7

Sequence 7, Application US/08993424B

LENGTH: 835
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: CD97amino acid sequence encoded by full-length
US-09-284-819-6

Query Match 5.0%; Score 98; DB 4; Length 835;
Best Local Similarity 22.8%; Pred. No. 0.23;
Matches 74; Conservative 50; Mismatches 118; Indels 82; Gaps 19;

QY 67 GAVGLGCGFMPTAYLLAISFLKPYQ---AAVAVIMGCCPGGTTISNIFTEWVD-- 120
DB 554 GLAALFLPL--LGLLTLFL-----VRPIQSRTHHLCCLRVG--STIFLAGIENE 604
QY 121 -GDMDLSISMTCTSVAAIGMPLCIYLYTWSW-SIQONLTPYONIGITVLCLTPAVF 178
DB 605 GGQVGL---RCRIYVA--GLIHYC-FLAALFCMSLE-----GIELYFLVAVYFQ 646
QY 179 GVVAVYRMPKSKIIKIGAVVGVLLVAVAVAGVVLAKGSNSDITLTI--SFIPLI 236
DB 647 GGLSTRW-----LCLIGY---GVPLLIVGVSAIYSGYRPRYCWIDFQGLWSFL 697
QY 237 GAVTGFEL---ALFTHQSQRCTISLETGAONIQCITMLO---LSFTAEHLVOMLSF 289
DB 698 GPTFTIICNAYIFVTYWKLVOKFS-----EINPMKKLKKARALTTTALQPLFLOC 751
QY 290 PLAYGLFQIDGFLVAAVOT-----YKRLKNRHK-----KNSGCT 327
DB 752 TWVFGIFEDDSLVLTVVFTILNCLQAFVLYLHCLLNKRYEEYRKACVLAVGSKYS 811
QY 328 EVCYTRKTSSTRETNALFEVNEEG 351
DB 812 EFTSTTSGTHNQTRA-LRASSG 834

RESULT 13

US-08-477-451-4
Sequence 4, Application US/08477451
Patent No. 592865
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori CagI Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chilton Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3177 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-4

Query Match 4.9%; Score 96.5; DB 2; Length 3177;
Best Local Similarity 21.9%; Pred. No. 2.2;
Matches 56; Conservative 35; Mismatches 62; Indels 103; Gaps 12;

QY 106 CPGGISNIFTEWVDGMDLSISMTCTSV---AALGM-----MPLCIYLYT 149
DB 57 CLKAYLSLTFWFI---LISLNTVSVKIRYSLGMPKLKLAITLGLPSCLRTF- 111
QY 150 WWSLSQONLTPYONIGITVCL---TIPVA--GVVAVYRMPKSKIIKIGAVVGV 204
DB 112 ---LSSPLVWISNSFSVTLNLSERLPSPFLKKIFVGH---CSLIVSAIGAKRSVM 163
QY 205 LLVAVAGVVLAKGSNSDITLTLISFIPLIGHVTFGLALFTHQSQRCTISLETGA 264
DB 164 L-----VASLTIAPLF-----LAVFS----- 179
QY 265 QNIQMCIT---MQLSFTAEHLVOMLSFPLAYGLFQIDGFLVAAVOTYKRLKNRKH 319
DB 180 ---NSLTKATPGSINTISRLHQLRYAHPPLG-----YERKGNKR 219
QY 320 GKNSGCTEVCYTRKS 335
DB 220 AKHHYCLANLHOROS 235

RESULT 14

US-08-956-322-4
Sequence 4, Application US/08956322
Patent No. 6277977
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,322
FILING DATE: 23-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,329
FILING DATE: 11-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-956-322-4

Query Match 4.9%; Score 96; DB 4; Length 521;
Best Local Similarity 19.3%; Pred. No. 0.19;
Matches 82; Conservative 52; Mismatches 107; Indels 184; Gaps 22;

4 NC---SSSSACPNSSSEELPVGLEVHGNLELFTVSTVMGLMFLSGCSVEIRKMS 60
203 NCSHLSFAVLMALTSQEDP-----VLTVITYV----- 231
61 HIRRPWGIAVGLTCQGLMPFTAYLLAISPFLKPVQAIIVLMGCCPGGTISNIFPMWD 120
232 ---GLSVSLC-----LLAALFTL-----CK--AIQNTST----- 258
121 GMDLISMTTCTVAALGMM-----PLC-----IYLYTWSMSL----- 154
259 ---SLHQLSLCFLHMLFLVGLIDRTEPKVLSIIAGALHYLLAFLAFTMLLEGVHLFL 315
155 -QONLT-IPYONIGITLVCLTIPVAGVYVNYRMPKOSKIIKIGAVGVLLVAVAG 212
316 TANNLVVNVSSINRLMKIMFPVYG-----VPAVT 347
213 VVLAKGSM-----NSDITLLTI--SFIFPLIGHVTGFL--LALFTHOSW----- 252
348 VAISAASWPHLYGTARCMHLHDOCFMMSFLGPVCAIFSANLVFLVFLVILKRLKSILN 407
253 -----QRCRTISLETGAQ-----NIQWCTIMQLSFTAEHLVOMLSFPLAYGLFOLID-- 300
408 SEVSTIQNRMFLAFKATAQLFLIGCTWCLGLLQVGPAAQ-----VNAV-LFTIINSI 458
301 -GFLIYAAVQTYRRLKXNGK-----KNSGCEVCHTRKSTSSRETNALFVNEG 351
459 QGFIFLVYCLLSQVQVQKQVREIVKSKSESEYTLSSKXGPKDSKPS-----EG 510
QY 352 AIRPG 356
DB 511 DVPPG 515

RESULT 15
US-08-937-067-13
Sequence 13, Application US/08937067
Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umanaky, Samuel
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067.
FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-13

Query Match 4.9%; Score 96; DB 4; Length 572;
Best Local Similarity 21.9%; Pred. No. 0.22;
Matches 57; Conservative 40; Mismatches 79; Indels 84; Gaps 13;

40 VMGGLMFLSGCSVEIRKMSHIRRPWGIAVGLTCQGLMPFTAYLLAISPFLKPVQ 96
337 LFMVLYFFGMASSI-----WVILSLTWFLAAGM--KMGHEALEANSQYFHLAAMAVPAVK 390
97 AIAVLIMGCCPGGTISNIFPMWDGMDLISMTTCTVAALG---MMPLCIYLYTWSMS 153
391 TITILAMG-----QVDDLSGVCYVGLSSVDALRGVLAFLFYLF----- 432
154 LQONLTIPYONIGITLVCLTIPVAGV-----YVNYRMPKOSKIIKIGAVGVLLV 208
433 -----IGTSFLAGFVSLFRIRIMGHDGTEKLEKLVRLG--VFSVLYTV 479
209 AVAGVLA-----KGSW-----NSDITLLTISIFPLI 236
480 AT--IVLACYFEQAQREHMERWTLLQTCASYAVPCPRHFSPMSPDFVFMKYLMTMI 537
QY 237 -GHVTF--LALFTHOSMOR 254
DB 538 VGITTFMWSGKTLQSMR 557

Search completed: June 9, 2003, 07:10:42
Job time : 21 secs